

ITERATED TEST OF THE HYPOTHESIS OF NO REGRESSION

Query by Hugh Graham
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Abstract

Taxonomic discrimination among species of primitive segmented organisms such as tapeworms are based in part on the morphometric traits of individual segments. The taxonomic utility of such traits is dependent upon the fact that segment dimensions become stable as total body length increases. A statistical procedure for determining the minimal body length required for segment stability is proposed, using an iterated hypothesis testing procedure developed by R. V. Hogg.

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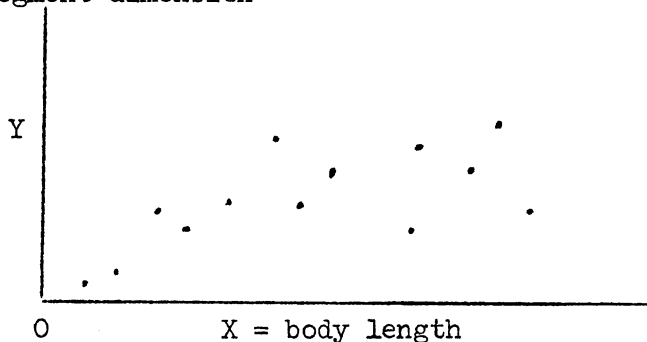
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In a search for morphometric traits which are independent of body length in a species of tapeworm it was found that for many traits Y the relation between Y and $X = \text{body length}$ took the form:

$Y = \text{body segment dimension}$



suggesting that beyond some minimal body length the characteristics of body segments are independent of body length.

The question of determining a cutoff point was viewed as the problem of testing iteratively for each observed value of X_i the hypothesis that for $x > X_i$ the regression function $E(Y|x)$ is a constant. Applying a principle given by R. V. Hogg (1962 JASA) we order the Y sample Y_1, Y_2, \dots, Y_n according to body length, $X_1 > X_2 > \dots > X_n$, then compute the Helmert statistics:

$$H_1 = \frac{Y_1 - Y_2}{\sqrt{2}} \quad , \quad H_2 = \frac{Y_1 + Y_2 - 2Y_3}{\sqrt{6}} \quad , \quad \dots \quad , \quad H_k = \frac{Y_1 + \dots + Y_k - kY_{k+1}}{\sqrt{k(k+1)}} \quad , \quad \dots$$

and then perform the sequence of independent F tests:

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$$F(1,1) = \frac{H_2^2}{H_1^2}$$

$$F(1,2) = \frac{2H_3^2}{H_1^2 + H_2^2}$$

⋮

$$F(1,k) = \frac{kH_{k+1}^2}{H_1^2 + \dots + H_k^2}$$

⋮

each at significant level $1 - (1-\alpha)^{\frac{1}{n-2}}$, in order to achieve a significance level α for the complete process. The smallest value of k such that $F(1,k)$ is significant determines X_{k+1} as a lower bound on the cutoff point.